

AC

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/914,541

DATE: 01/15/2002
 TIME: 13:04:25

Input Set : A:\09914541.app
 Output Set: N:\CRF3\01152002\I914541.raw

ENTERED

3 <110> APPLICANT: THE UNIVERSITY OF TENNESSEE RESEARCH CORPORATION
 4 BECKER, JEFFREY M.
 5 HAUSER, MELINDA
 6 DONHARDT, AMY
 7 BARNES, DAVID
 9 <120> TITLE OF INVENTION: EUKARYOTIC PEPTIDE UPTAKE SYSTEM FOR TRANSPORTING
 10 ENKEPHALINS
 12 <130> FILE REFERENCE: 1046-PCT-00
 14 <140> CURRENT APPLICATION NUMBER: 09/914541
 15 <141> CURRENT FILING DATE: 2001-08-29
 17 <150> PRIOR APPLICATION NUMBER: PCT/US00/05158
 18 <151> PRIOR FILING DATE: 2000-03-01
 20 <150> PRIOR APPLICATION NUMBER: 60/122,312
 21 <151> PRIOR FILING DATE: 1999-03-01
 23 <160> NUMBER OF SEQ ID NOS: 26
 25 <170> SOFTWARE: PatentIn Ver. 2.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 2400
 29 <212> TYPE: DNA
 30 <213> ORGANISM: *Saccharomyces cerevisiae*
 32 <400> SEQUENCE: 1
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 34 accattccta tccagatcaa tatggaagag gaaaagaaag atgcgttctgt taagaatatt 120
 35 gacgaggacg tcaataatct cactgcgact actgtatgagg aggacccgca tccggaaagc 180
 36 caaaaattcg acaggcattc catacaggag gaaggctcg tttgaaaggg cgaccctaca 240
 37 tacttgccca attctccata tcctgaagtg agatccgcgg tgtccatcga ggatgacccc 300
 38 accatccgccc tcaaccactg gagaacgtgg ttcttgacca cggtgtttgt ggttagtttc 360
 39 gccggtgtta atcaattttt ttccctgaga tatccatcgc tagagatcaa ctccctgtt 420
 40 gcacaagttt tttgctaccc aattggtagg atactggctc tcttgcggca ctggaaagtgt 480
 41 tctaaagtgc cattttcga tttaaacccg ggcccatatta caaaaaagga acacgccgtg 540
 42 gtcacaatttgc cctgtggcgct tacttcctct actgcatacg ctatgtacat ttgaacgcc 600
 43 cagggaaagct tttacaacat gaaacttaat gtcggatatac agttttgtt ggtttggaca 660
 44 tctcaaatttga ttggtttatgg tgctgcaggt cttaccagaa gatgggtcgtaaaccctgca 720
 45 agctctatct ggcctcagac tttaatttca gtgtccttgt ttgattcggt gcactcgaga 780
 46 aaagttgaaa agacagtgc aatgggttg acgatcccc gttacaggtt cttcttaatc 840
 47 gtccttatcg gatcgatcat ctggattttgg gtacctggat ttctcttac cggctgtcc 900
 48 tatttcaacg ttatccatg ggggtcgaag acaagacaca atttcatcgc taacacaatc 960
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 51 tcagtgttga tattctctgt catagtgcgtt ccatgtcttt attttacgaa tacctggat 1140
 52 gccaaataca tgcccgatcat ttccaggatct acttatgaca acactcaaaa caaatacaac 1200
 53 gtaacaaaga ttcttaacga ggattattcc attaatctt agaaatataa ggaataactca 1260
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 55 gccgttttttgc tccactgcat ctataccac ggttaaagata ttgtcgccaa gttaaagac 1380
 56 cgtaaaaatgc gttggactga cattcacatg agaatctact ccaagaacta taaggattgt 1440
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 58 tgcgttttcg atactaagtt cccagcttgc gcatattgttta ttgcaatatt aattttccctt 1560

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59 gtaaatttca tcccgaagg tatcttgaa gcaatgacta accaacacgt aggttgaat 1620
 60 attatcacag aattgatctg cggttatatg ctgcctttaa gaccaatggc aaacttatta 1680
 61 ttcaagctat acggatttat tgtcatgaga caaggcttga atttgagtag agattgaaa 1740
 62 tttagccatgt acatgaaggt ttccccctcg ttgatcttg cggttcaaattt ctatgccact 1800
 63 atcatatcag gcatggtaa cgttgggttc caggaatgga tgatgcataa tatcgatggc 1860
 64 ttatgtacca ccgatcaacc aaatggcttc acttgtgcta atggtcgcac ggtttcaat 1920
 65 gcttccattha tctggcttt gccaaagtat cttttctcat cagggcgcattt ttataatccg 1980
 66 ctgatgtggc tcttcttgat tggttgcta ttcccactag cggttatgc tggtaatgg 2040
 67 aaattcccta aatttaattt tgctaagcac attcataactc ctgtatTTT cacaggccca 2100
 68 ggttaatattc caccaagcac accttataac tactcattat ttttgcaat gtcattctgc 2160
 69 ctaaaacttga taagaaaaag atggagagct tggttcaata agtacaattt cgtcatgggg 2220
 70 gccgggtttt aagcaggtgt gcaatctcc gtcgtcatca tcttcttggt tgtaacgtac 2280
 71 ccaggtggta agctcagctg gtggggaaac aacgtttggaa aagaacgta tgataatgtat 2340
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 76 <211> LENGTH: 799
 77 <212> TYPE: PRT
 78 <213> ORGANISM: Saccharomyces cerevisiae
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 82 1 5 10 15
 84 Pro Thr Pro Thr Thr Ile Pro Ile Gln Ile Asn Met Glu Glu Glu Lys
 85 20 25 30
 87 Lys Asp Ala Phe Val Lys Asn Ile Asp Glu Asp Val Asn Asn Leu Thr
 88 35 40 45
 90 Ala Thr Thr Asp Glu Glu Asp Arg Asp Pro Glu Ser Gln Lys Phe Asp
 91 50 55 60
 93 Arg His Ser Ile Gln Glu Glu Gly Leu Val Trp Lys Gly Asp Pro Thr
 94 65 70 75 80
 96 Tyr Leu Pro Asn Ser Pro Tyr Pro Glu Val Arg Ser Ala Val Ser Ile
 97 85 90 95
 99 Glu Asp Asp Pro Thr Ile Arg Leu Asn His Trp Arg Thr Trp Phe Leu
 100 100 105 110
 102 Thr Thr Val Phe Val Val Val Phe Ala Gly Val Asn Gln Phe Phe Ser
 103 115 120 125
 105 Leu Arg Tyr Pro Ser Leu Glu Ile Asn Phe Leu Val Ala Gln Val Val
 106 130 135 140
 108 Cys Tyr Pro Ile Gly Arg Ile Leu Ala Leu Leu Pro Asp Trp Lys Cys
 109 145 150 155 160
 111 Ser Lys Val Pro Phe Phe Asp Leu Asn Pro Gly Pro Phe Thr Lys Lys
 112 165 170 175
 114 Glu His Ala Val Val Thr Ile Ala Val Ala Leu Thr Ser Ser Thr Ala
 115 180 185 190
 117 Tyr Ala Met Tyr Ile Leu Asn Ala Gln Gly Ser Phe Tyr Asn Met Lys
 118 195 200 205
 120 Leu Asn Val Gly Tyr Gln Phe Leu Leu Val Trp Thr Ser Gln Met Ile
 121 210 215 220
 123 Gly Tyr Gly Ala Ala Gly Leu Thr Arg Arg Trp Val Val Asn Pro Ala
 124 225 230 235 240

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126 Ser Ser Ile Trp Pro Gln Thr Leu Ile Ser Val Ser Leu Phe Asp Ser
127 245 250 255
129 Leu His Ser Arg Lys Val Glu Lys Thr Val Ala Asn Gly Trp Thr Met
130 260 265 270
132 Pro Arg Tyr Arg Phe Phe Leu Ile Val Leu Ile Gly Ser Phe Ile Trp
133 275 280 285
135 Tyr Trp Val Pro Gly Phe Leu Phe Thr Gly Leu Ser Tyr Phe Asn Val
136 290 295 300
138 Ile Leu Trp Gly Ser Lys Thr Arg His Asn Phe Ile Ala Asn Thr Ile
139 305 310 315 320
141 Phe Gly Thr Gln Ser Gly Leu Gly Ala Leu Pro Ile Thr Phe Asp Tyr
142 325 330 335
144 Thr Gln Val Ser Gln Ala Met Ser Gly Ser Val Phe Ala Thr Pro Phe
145 340 345 350
147 Tyr Val Ser Ala Asn Thr Tyr Ala Ser Val Leu Ile Phe Phe Val Ile
148 355 360 365
150 Val Leu Pro Cys Leu Tyr Phe Thr Asn Thr Trp Tyr Ala Lys Tyr Met
151 370 375 380
153 Pro Val Ile Ser Gly Ser Thr Tyr Asp Asn Thr Gln Asn Lys Tyr Asn
154 385 390 395 400
156 Val Thr Lys Ile Leu Asn Glu Asp Tyr Ser Ile Asn Leu Glu Lys Tyr
157 405 410 415
159 Lys Glu Tyr Ser Pro Val Phe Val Pro Phe Ser Tyr Leu Leu Ser Tyr
160 420 425 430
162 Ala Leu Asn Phe Ala Ala Val Ile Ala Val Phe Val His Cys Ile Leu
163 435 440 445
165 Tyr His Gly Lys Asp Ile Val Ala Lys Phe Lys Asp Arg Lys Asn Gly
166 450 455 460
168 Gly Thr Asp Ile His Met Arg Ile Tyr Ser Lys Asn Tyr Lys Asp Cys
169 465 470 475 480
171 Pro Asp Trp Trp Tyr Leu Leu Leu Gln Ile Val Met Ile Gly Leu Gly
172 485 490 495
174 Phe Val Ala Val Cys Cys Phe Asp Thr Lys Phe Pro Ala Trp Ala Phe
175 500 505 510
177 Val Ile Ala Ile Leu Ile Ser Leu Val Asn Phe Ile Pro Gln Gly Ile
178 515 520 525
180 Leu Glu Ala Met Thr Asn Gln His Val Gly Leu Asn Ile Ile Thr Glu
181 530 535 540
183 Leu Ile Cys Gly Tyr Met Leu Pro Leu Arg Pro Met Ala Asn Leu Leu
184 545 550 555 560
186 Phe Lys Leu Tyr Gly Phe Ile Val Met Arg Gln Gly Leu Asn Leu Ser
187 565 570 575
189 Arg Asp Leu Lys Leu Ala Met Tyr Met Lys Val Ser Pro Arg Leu Ile
190 580 585 590
192 Phe Ala Val Gln Ile Tyr Ala Thr Ile Ile Ser Gly Met Val Asn Val
193 595 600 605
195 Gly Val Gln Glu Trp Met Met His Asn Ile Asp Gly Leu Cys Thr Thr
196 610 615 620
198 Asp Gln Pro Asn Gly Phe Thr Cys Ala Asn Gly Arg Thr Val Phe Asn

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Input Set : A:\09914541.app
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199	625	630	635	640
201	Ala Ser Ile Ile Trp Ser Leu Pro Lys Tyr	Leu Phe Ser Ser Gly	Arg	
202	645	650	655	
204	Ile Tyr Asn Pro Leu Met Trp Phe	Phe Leu Ile Gly	Leu Leu Phe Pro	
205	660	665	670	
207	Leu Ala Val Tyr Ala Val Gln Trp Lys	Phe Pro Lys Phe	Lys Phe Ala	
208	675	680	685	
210	Lys His Ile His Thr Pro Val Phe	Phe Thr Gly	Pro Gly Asn Ile Pro	
211	690	695	700	
213	Pro Ser Thr Pro Tyr Asn Tyr Ser Leu Phe	Phe Ala Met Ser Phe Cys		
214	705	710	715	720
216	Leu Asn Leu Ile Arg Lys Arg Trp Arg	Ala Trp Phe Asn Lys Tyr Asn		
217	725	730	735	
219	Phe Val Met Gly Ala Gly Val Glu Ala	Gly Val Ala Ile Ser Val Val		
220	740	745	750	
222	Ile Ile Phe Leu Cys Val Gin Tyr Pro	Gly Gly Lys Leu Ser Trp Trp		
223	755	760	765	
225	Gly Asn Asn Val Trp Lys Arg Thr Tyr Asp Asn	Asp Tyr Lys Lys Phe		
226	770	775	780	
228	Tyr Thr Leu Lys Lys Gly Glu Thr Phe	Gly Tyr Asp Lys Trp Trp		
229	785	790	795	
232	<210> SEQ ID NO: 3			
233	<211> LENGTH: 753			
234	<212> TYPE: PRT			
235	<213> ORGANISM: Arabidopsis thaliana			
237	<400> SEQUENCE: 3			
238	Met Val Gly Ser Leu Glu Val Ser Lys Pro Pro Glu His Lys Val Glu			
239	1	5	10	15
241	Ser Lys Ile Val Ile Ala Asp Glu Glu Glu Asp Glu Asn Asp Ser			
242	20	25	30	
244	Pro Ile Glu Glu Val Arg Leu Thr Val Pro Ile Thr Asp Asp Pro Ser			
245	35	40	45	
247	Leu Pro Val Leu Thr Phe Arg Thr Trp Phe Leu Gly Met Val Ser Cys			
248	50	55	60	
250	Val Val Leu Ala Phe Val Asn Asn Phe	Gly Tyr Arg Ser Asn Pro		
251	65	70	75	80
253	Leu Thr Val Ser Ser Val Val Ala Gln Ile Ile Thr Leu Pro Leu Gly			
254	85	90	95	
256	Lys Leu Met Ala Thr Thr Leu Pro Thr Thr Lys Leu Arg Leu Pro Gly			
257	100	105	110	
259	Thr Asn Trp Ser Cys Ser Leu Asn Pro Gly Pro Phe Asn Met Lys Glu			
260	115	120	125	
262	His Val Leu Ile Thr Ile Phe Ala Asn Thr Gly Ala Gly Gly Ala Tyr			
263	130	135	140	
265	Ala Thr Ser Ile Leu Thr Ile Val Lys Ala Phe Tyr His Arg Asn Leu			
266	145	150	155	160
268	Asn Pro Ala Ala Ala Met Leu Leu Val Gln Thr Thr Gln Leu Leu Gly			
269	165	170	175	
271	Tyr Gly Trp Ala Gly Met Phe Arg Lys Tyr Leu Val Asp Ser Pro Tyr			

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272	180	185	190	
274	Met Trp Trp Pro Ala Asn Leu Val Gln Val Ser Leu Phe Arg Ala Leu			
275	195	200	205	
277	His Glu Lys Glu Glu Lys Arg Glu Gly Lys Gln Thr Lys Leu Arg Phe			
278	210	215	220	
280	Phe Leu Ile Val Phe Phe Leu Ser Phe Thr Tyr Tyr Ile Val Pro Gly			
281	225	230	235	240
283	Tyr Leu Phe Pro Ser Ile Ser Tyr Leu Ser Phe Val Cys Trp Ile Trp			
284	245	250	255	
286	Thr Arg Ser Val Thr Ala Gln Gln Ile Gly Ser Gly Leu His Gly Leu			
287	260	265	270	
289	Gly Ile Gly Ser Phe Gly Leu Asp Trp Ser Thr Val Ala Gly Phe Leu			
290	275	280	285	
292	Gly Ser Pro Leu Ala Val Pro Phe Phe Ala Ile Ala Asn Ser Phe Gly			
293	290	295	300	
295	Gly Phe Ile Ile Phe Phe Tyr Ile Ile Leu Pro Ile Phe Tyr Trp Ser			
296	305	310	315	320
298	Asn Ala Tyr Glu Ala Lys Lys Phe Pro Phe Tyr Thr Ser His Pro Phe			
299	325	330	335	
301	Asp His Thr Gly Gln Arg Tyr Asn Thr Thr Arg Ile Leu Asn Gln Lys			
302	340	345	350	
304	Thr Phe Asn Ile Asp Leu Pro Ala Tyr Glu Ser Tyr Ser Lys Leu Tyr			
305	355	360	365	
307	Leu Ser Ile Leu Phe Ala Leu Ile Tyr Gly Leu Ser Phe Gly Thr Leu			
308	370	375	380	
310	Thr Ala Thr Ile Ser His Val Ala Leu Phe Asp Gly Lys Phe Ile Trp			
311	385	390	395	400
313	Glu Leu Trp Lys Lys Ala Thr Leu Thr Thr Lys Asp Lys Phe Gly Asp			
314	405	410	415	
316	Val His Thr Arg Leu Met Lys Lys Asn Tyr Lys Glu Val Pro Gln Trp			
317	420	425	430	
319	Trp Phe Val Ala Val Leu Ala Ala Ser Phe Val Leu Ala Leu Tyr Ala			
320	435	440	445	
322	Cys Glu Gly Phe Gly Lys Gln Leu Gln Leu Pro Trp Trp Gly Leu Leu			
323	450	455	460	
325	Leu Ala Cys Ala Ile Ala Phe Thr Phe Thr Leu Pro Ile Gly Val Ile			
326	465	470	475	480
328	Leu Ala Thr Thr Asn Gln Arg Met Gly Leu Asn Val Ile Ser Glu Leu			
329	485	490	495	
331	Ile Ile Gly Phe Leu Tyr Pro Gly Lys Pro Leu Ala Asn Val Ala Phe			
332	500	505	510	
334	Lys Thr Tyr Gly Ser Val Ser Ile Ala Gln Ala Leu Tyr Phe Val Gly			
335	515	520	525	
337	Asp Phe Lys Leu Gly His Tyr Met Lys Ile Pro Pro Arg Ser Met Phe			
338	530	535	540	
340	Ile Val Gln Leu Val Ala Thr Ile Val Ala Ser Thr Val Ser Phe Gly			
341	545	550	555	560
343	Thr Thr Trp Trp Leu Leu Ser Ser Val Glu Asn Ile Cys Asn Thr Asp			
344	565	570	575	

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\09914541.app

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L:2570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24

L:2599 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26

L:2599 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26

L:2599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26